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OM protein - protein search, using sw model

Run on: June 9, 2003, 07:07:25 ; Search time 19 Seconds
(without alignments)
583.813 Million cell updates/sec

Title: US-10-091-628-2
Perfect score: 1979
Sequence: 1 MRANSSSSACAPNSSEEL.....PGPMCHRALPVGHTSCB 377

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
ched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 10%
Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	884	44.7	348	1	US-08-176-126B-2
2	884	44.7	348	2	US-08-669-435-2
3	884	44.7	348	5	PCT-US94-14431A-2
4	860.5	43.5	348	1	US-08-176-126B-4
5	860.5	43.5	348	2	US-08-669-435-4
6	860.5	43.5	348	5	PCT-US94-14431A-4
7	101	5.1	370	4	US-08-405-271A-21
8	100.5	5.1	424	4	US-09-134-001C-5009
9	99.5	5.0	387	4	US-08-993-088A-7
10	99.5	5.0	387	4	US-08-993-424B-7
11	98.5	5.0	344	3	US-09-110-116-4
12	98	5.0	835	4	US-09-284-819-6
13	96.5	4.9	3177	2	US-08-477-451-4
14	96	4.9	521	4	US-08-956-322-4
15	96	4.9	572	4	US-08-937-067-13
16	96	4.9	652	4	US-09-110-116-1
17	95	4.9	652	4	US-08-956-322-2
18	93	4.7	372	2	US-08-514-451A-9
19	93	4.7	372	4	US-09-048-916B-8
20	93	4.7	487	1	US-08-444-734A-2
21	93	4.7	532	1	US-08-140-729A-3
22	93	4.7	532	1	US-08-546-666-3
23	93	4.7	532	2	US-08-916-745-3
24	93	4.7	532	2	US-09-042-923-3
25	93	4.7	532	2	US-08-546-661-3
26	93	4.7	532	2	US-09-042-960-3
27	93	4.7	532	3	US-09-198-650-3

28	93	4.7	532	3	US-09-042-913-3	Sequence 3, Appli
29	93	4.7	532	3	US-09-042-937-3	Sequence 3, Appli
30	93	4.7	532	4	US-09-042-709A-3	Sequence 3, Appli
31	92.5	4.7	554	4	US-09-134-001C-5109	Sequence 3109, Ap
32	92	4.6	683	4	US-09-134-001C-5576	Sequence 5576, Ap
33	91.5	4.6	367	2	US-08-454-549-4	Sequence 4, Appli
34	91.5	4.6	367	2	US-08-454-552-4	Sequence 4, Appli
35	91.5	4.6	367	3	US-08-676-351-3	Sequence 3, Appli
36	91.5	4.6	372	4	US-08-188-275A-4	Sequence 4, Appli
37	91.5	4.6	372	4	US-09-351-198-4	Sequence 4, Appli
38	91.5	4.6	372	4	US-09-113-426-4	Sequence 4, Appli
39	91.5	4.6	485	1	US-08-453-956-15	Sequence 15, Appli
40	91.5	4.6	485	1	US-08-086-631-15	Sequence 15, Appli
41	91.5	4.6	485	2	US-08-452-930-15	Sequence 15, Appli
42	91.5	4.6	485	5	PCT-US93-08174-15	Sequence 15, Appli
43	91	4.6	843	4	US-09-361-631-1	Sequence 1, Appli
44	90.5	4.6	405	4	US-09-134-001C-4999	Sequence 4999, Ap
45	90	4.5	372	3	US-09-170-331-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-08-176-126B-2
Sequence 2- Application US/08176126B
Patent No. 5589358

GENERAL INFORMATION:

APPLICANT: Dawson, Paul A.

TITLE OF INVENTION: IDEAL BILE ACID TRANSPORTER COMPOSITIONS AND

METHODS

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESS: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: Texas

COUNTRY: US

ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/176,126B

FILING DATE: 29-DEC-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Parker, David L.

REGISTRATION NUMBER: 32,165

REFERENCE/DOCKET NUMBER: WAKE:002/PAR

TELECOMMUNICATION INFORMATION:

TELEPHONE: (512) 418-3000

TELEFAX: (512) 474-7577

TELEX: na

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 348 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-176-126B-2

Query Match 44.7% ; Score 884 ; DB 1 ; Length 348 ;
Best Local Similarity 46.9% ; Pred. No. 2.4e-82 ;
Matches: 164 ; Conservative 74 ; Mismatches 102 ; Indels 10 ; Gaps 4 ;

QY 7 SSSACPNSS--EEELPVGLEVHGN--LELVFTVSTVMGLMPSLCCSVETKLNHSHI 62
DB 3 NSSICNPATICEGDSICAPNSFNALISVMSYTLITLALVMSQCNELKHFLOLH 62
QY 63 RRPWGIAVGLICQGLMPFTAYLLAISFLKPVQAVIAVLINGCCPGGITSNIFFWVDGD 122

Db 63 RRPWGIIVGFLCQFGIMPLTGFLVAVAFGILPVQAVVLIQCCPGGTAISNLAIVWDGD 122
Qy 123 MDLSIMTCTSTVALGMPPLCIYLYTWSMSLQONLTIPYONIGITLVCLTIPVAFGVV 182
Db 123 MDLSVMTCTSTLALGMPPLCIYLYTWSMSLQONLTIPYONIGITLVCLTIPVAFGVV 182
Qy 183 NYRMPKOSKIIILKIGAVGVLLVAVAVGLAKGSNSDITLLTISIFPLIGHVTGF 242
Db 183 NYRMPKOSKIIILKIGAVGVLLVAVAVGLAKGSNSDITLLTISIFPLIGHVTGF 242
Qy 243 LLALFTHSQWRCRTISLFTGAONIQMTLMQSTAEHLVOMLSFPLAVGLPOLIDGF 302
Db 243 FLARIAGQPMYRCRVALLETGLONTQLCSTIVQLSFSFEDLNLVFTFPLIYSIFQIAFPA 302
Qy 303 LIVAAYQTYKRLKNHKGKNSGCTEVCHTRKS--TSRETNALFEVNEE 350
Db 303 ILGAVVAYKK-----CHGKNNTLEOKTDNEMEPRSSFOETNKGQFPDEK 348

ULT 2

08-669-435-2
Sequence 2, Application US/08669435

Patent No. 5869265

GENERAL INFORMATION:

APPLICANT: Dawson, Paul A.

TITLE OF INVENTION: IDEAL BILE ACID TRANSPORTER COMPOSITIONS AND

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: Texas

COUNTRY: US

ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/669,435

FILING DATE: 26-JUN-1996

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/176,126

FILING DATE: 29-DEC-1993

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Parker, David L.

REGISTRATION NUMBER: 32,165

REFERENCE/DOCKET NUMBER: WAKE:002/PAW

TELECOMMUNICATION INFORMATION:

TELEPHONE: (512) 418-3000

TELEFAX: (512) 474-7577

TELEX: na

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 348 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-669-435-2

Query Match 44.7%; Score 884; DB 2; Length 348;

Best Local Similarity 46.9%; Pred. NO. 2.4e-82;

Matches 164; Conservative 74; Mismatches 102; Indels 10; Gaps 4;

Qy 7 SSSACPNANS--EEELPVGLEVHGN--LELVFTVSTVMGMLMGLSGVSEIRKLSHI 62
Db 3 NSSICNPNTICGDSICIAESNPNALISVVMSTVLTLLALVMSGCVNELHRTFLGHL 62

Qy 63 RRPWGIIVGFLCQFGIMPLTGFLVAVAFGILPVQAVVLIQCCPGGTAISNLAIVWDGD 122
Db 63 RRPWGIIVGFLCQFGIMPLTGFLVAVAFGILPVQAVVLIQCCPGGTAISNLAIVWDGD 122
Qy 123 MDLSIMTCTSTVALGMPPLCIYLYTWSMSLQONLTIPYONIGITLVCLTIPVAFGVV 182
Db 123 MDLSVMTCTSTLALGMPPLCIYLYTWSMSLQONLTIPYONIGITLVCLTIPVAFGVV 182
Qy 183 NYRMPKOSKIIILKIGAVGVLLVAVAVGLAKGSNSDITLLTISIFPLIGHVTGF 242
Db 183 NYRMPKOSKIIILKIGAVGVLLVAVAVGLAKGSNSDITLLTISIFPLIGHVTGF 242
Qy 243 LLALFTHSQWRCRTISLFTGAONIQMTLMQSTAEHLVOMLSFPLAVGLPOLIDGF 302
Db 243 FLARIAGQPMYRCRVALLETGLONTQLCSTIVQLSFSFEDLNLVFTFPLIYSIFQIAFPA 302
Qy 303 LIVAAYQTYKRLKNHKGKNSGCTEVCHTRKS--TSRETNALFEVNEE 350
Db 303 ILGAVVAYKK-----CHGKNNTLEOKTDNEMEPRSSFOETNKGQFPDEK 348

RESULT 3

PCT-US94-14431A-2
Sequence 2, Application PC/TUS9414431A

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: IDEAL BILE ACID TRANSPORTER COMPOSITIONS

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: Texas

COUNTRY: United States of America

ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII

SOFTWARE: Patentin Release #1.0, Version

SOFTWARE: #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/14431A

FILING DATE: 29-DEC-1994

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USN 08/176,126

FILING DATE: 29-DEC-1993

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: PARKER, DAVID L.

REGISTRATION NUMBER: 32,165

REFERENCE/DOCKET NUMBER: WAKE005P--

TELECOMMUNICATION INFORMATION:

TELEPHONE: (512) 418-3000

TELEFAX: (713) 789-2679

TELEX: 79-0924(1) GENERAL INFORMATION:

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 348 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US94-14431A-2

Query Match 44.7%; Score 884; DB 5; Length 348;

Best Local Similarity 46.9%; Pred. NO. 2.4e-82;

Matches 164; Conservative 74; Mismatches 102; Indels 10; Gaps 4;

Qy 7 SSSACPNANS--EEELPVGLEVHGN--LELVFTVSTVMGMLMGLSGVSEIRKLSHI 62
Db 3 NSSICNPNTICGDSICIAESNPNALISVVMSTVLTLLALVMSGCVNELHRTFLGHL 62

RESULT 4
DS-08-176-126B-4
Sequence 4 Application US/08176126B

CORRESPONDENCE ADDRESS:
* ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: US
ZIP: 77210

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: Patent Release #1.0, Version #1.25B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/176,126B
FILING DATE: 29-DEC-1993

ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,155
REFERENCE/DOCKET NUMBER: WAKE:002/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
TELEX: na
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
OS-09-176-126B-4

Query Match	Score	DB 1	Length
Best Local Similarity	860.5	DB 1	348
Matches 160; Conservative	68	Indels 19; Gaps 4	

QY C S S S S A C P A N S S E E L P G L E V H G N L E L Y T V T V S V M M G L M F S I G C V E R K L M S I R R 64
 14 C S G A S C V C P E S P N N I L S V L S T V L I L L A L V F S G N C V E L K F L G H K R 64
 Db
 QY P K G I A N G L C Q F G L M P F T A Y L L A I S F S L K P V A I A V L I M G C C P G S T I N I F T F V D G D M D 124
 65 P M G I C V G F L C Q F G I M P L T G I L S V A D I L P L A V V A V L I G C C P G G T A S I N I L A Y V D D M D 124

```

Qy 125 L5SMSTGCTVAALGMMPLCIYLWYMSLSLOONLIPONIGITVLCITIPVAGVYVY 184
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 125 L5VSMSTCTCTLALGMPCLLITRYRMVDSGSIYIPDNIGTSLVALVVPVSLGMYNH 184
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

Qy 185 RMRKSGKIILIKGAVGVYLLVVAAGVVLAKGWSNDITLLTISFIPPLIGHVTEFL 244
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Dh 185 KMPQKAKIILIKGISIGAILIVLIVVGGIILYQSAMITAPLWTIIGTIFPVAGSYSLFL 244
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

Qy 245 ALTHPSMQRCTTISLETGANOINQICIMLOLSPFAEHLVOMLSFPLAYGLFOLDGLI 304
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Dh 245 ARIAGLPWRCRIVFAVEGTOMTOLCSTIVOLSPFEEELNAVFFPPLIYSIFOLAPFAIF 304
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

Qy 305 VAAVQTYQTRRLNKKKGGKNGSGTEVCHTRKTSYSRETAFLVBEAGAITP 355
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Dh 305 LGTYVAVYKK-----CHOKNAEAIPE-----SKENGTEPSSFFKAN--GGFOP 345

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RESULT 5
US-08-669-435-4
; Sequence 4 - Application US/08669435
; Patent No. 7,466,002

```

1  TITLE O INVENTION: ILEAL BILE ACID TRANSPORTER COMPOSITIONS AND
2  TITLE OF INVENTION: METHODS
3  NUMBER OF SEQUENCES: 5
4  CORRESPONDENCE ADDRESS:
5  ADDRESSEE: Arnold, White & Durkee
6  STREET: P.O. Box 4433
7  CITY: Houston
8  STATE: Texas
9  COUNTRY: US
10 ZIP: 77210
11
12 COMPUTER READABLE FORM:
13 MEDIUM TYPE: Floppy disk
14 COMPUTER: IBM PC compatible
15 OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
16 SOFTWARE: PatentIn Release #1.0, Version #1.25
17 CURRENT APPLICATION DATA:
18 APPLICATION NUMBER: US/08/669,435
19 FILING DATE: 26-JUN-1996
20 CLASSIFICATION:
21 PRIOR APPLICATION DATA:
22 APPLICATION NUMBER: US 08/176,126
23 FILING DATE: 23-DEC-1993
24 CLASSIFICATION:
25 ATTORNEY/AGENT INFORMATION:
26 NAME: Parker, David L.
27 REGISTRATION NUMBER: 32,165
28 REFERENCE/DOCKET NUMBER: WAKE:002/PAR
29 TELECOMMUNICATION INFORMATION:
30 TELEPHONE: (512) 418-3000
31 TELEFAX: (512) 474-7577
32
33 TELEX: na
34 INFORMATION FOR SEQ ID NO: 4:
35 SEQUENCE CHARACTERISTICS:
36 LENGTH: 348 amino acids
37 TYPE: amino acid
38 TOPOLOGY: linear
39 MOLECULE TYPE: protein
40
41 US-08-669-435-4

```

Query Match	43.5%	Score 860.5	DB 2	Length 348
Best Local Similarly	45.6%	Pred. No. 6.2e-80		
Matches 160	Conservative 68	Mismatches 104	Indels 19	Gaps 4

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QY      5  CSSSSACPNASSSEELPVGLEVHGNLDELFTVYVTSVMMGLMFLSGCVERIKLMSIKR  64
      14  CSQSGCVPESESNFNNT-----LSVVLSTVLITLALVFMSCGVLEIKKELGIKIR  64
QY      65  PMGIATGLLQGRGLMFTVALIASFSLKPVQALAVLIMGCCPRGTSINITFTFVVDMD 124
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```


QY 58 LMSHRRPWGIAVGLLCOFGLMPTAYLALIS---PSLKPVOALVIMGCCPGTISNI 114
DB 62 -----GLIGNVLVWGVIVTRKMTATNIYIFNLALADALNSTL---PFSAKTL 109
QY 115 FTFVWDGMDLSISMTTSTVALGMPCLITYTWSWSLQONLITPYONIGITLVCLT- 173
DB 110 METWPFGEI-----LCKAV-----LSIDYNNMFTSIFITLM 140
QY 174 -----IVARGV-YVNRWPKOSKI---LKIGAVGVLVAVVA---GVLA--- 216
DB 141 MSVDRIYVCHPVALDFRTPAKALINICIVWLASGVGVPTWMAVTRPRDGAVVCMIQ 200
QY 217 --KGSWNSD---ITLITISFIFPLIGHVGTPLALFTHOSWQCRKISLETGAONIOMC 270
DB 201 FSPSPWMDTVTKICVPLFAFVPLIITVCGIML-----RARSVLSSGSKEXORS 254
QY 271 ---ITMLOSTFAEHLV---QMLSPPLAVGLFOLIDGLIYAAVGYTKRRLKNKKGKNS 324
DB 255 LRRITRMVLVVGAFCVVCAPFIHIVITVLDIRRDPLVVAAL-----HLCIALGVANS 309
QY 325 GCTEVCHTRKSTSSRETNAFLEVNREGAITP-----GPPGMDCHRALEPVG--HITSC 376
DB 310 SLNPLY-----AFIDENFKRCFRQLCRKPCGPPDSSPSRAEATAREBVTAAC 358

RESULT 8

US-09-134-001C-5009
; Sequence 5009, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5009
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5009

Query Match 5.1%; Score 100.5; DB 4; Length 424;
Best Local Similarity 28.4%; Pred. No. 0.05;
Matches 55; Conservative 30; Mismatches 74; Indels 35; Gaps 11;

QY 32 LVFTVSTVVMGLMFLSG-----CSVEIRKL-WSHIRRPW---GIVAGLCOFGLMPT 82
DB 228 LVFFIVAVVS---LLESTGVYHALSEITGRKLERDPRFGKYAEGIAIILGSIFFAFPT 284
QY 83 AY-----LLAISFSKRP---VQATAVIMGCCPG-GTISNFTFWV-DGMDLSISMTT 131
DB 255 AYSQNVGLVSGAKKNVITYGMVILLICGICPKLALANTIIPLVJGGAIAIAMEGMM 344
QY 132 CSTVALGMPCLITYTWSWSLQONLITPYONIGITLVCLTIPYAF-GVYVNRWPKOS 190
DB 345 AYGVSIILNI-----NFOONNLLIATISVGLAGISAVPAQFKGLSGQFAMLQON 395
QY 191 KIILKIGAVGVCL 204
DB 356 GIVL--GAISATIL 407

RESULT 9

US-08-993-088A-7
; Sequence 7, Application US/08993088A
; Patent No. 6287855
; GENERAL INFORMATION:

APPLICANT: Tan, Carina
APPLICANT: Sullivan, Kathleen
TITLE OF INVENTION: GALANIN RECEPTOR GALR2 AND
TITLE OF INVENTION: NUCLEOTIDES ENCODING SAME
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000, 126 E. Lincoln Ave.
CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065-0900

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,088A
FILING DATE: 18-DEC-1997
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/033,851
FILING DATE: 27-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 19846
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-1958
TELEFAX: 732-594-4720
TELEX:

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 387 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-993-088A-7

Query Match 5.0%; Score 99.5; DB 4; Length 387;
Best Local Similarity 20.8%; Pred. No. 0.056;
Matches 73; Conservative 47; Mismatches 118; Indels 113; Gaps 18;

QY 109 GTISN-IFTFWVDGMDLSISMTTCTSTVALGMPCLITYTWSWSLQONLITPYONIG 166
DB 39 GTVGNTVLAVILRGQAVS---TTNLFIMLGVALDLCFIL-----CVVFPQATI 85
QY 167 IT-----LVCLTI-----PVAFGVYVNRWPKOSK-----ITLK 195
DB 86 YTLDSWVSGSLCKAVHFLIFLTMWASSFTLAASLDRIYLRPLHSRELRTPRNALAA 145
QY 196 IGAVVGVLIL-----VVAAGVVLAKGSWNS-----DTLITISFIFPLIGHT 240
DB 146 IGLIMGSLSLSGPYLSYRROSQANLTVCHPANSAPRRAMDICTFVPSILPVL--VL 203
QY 241 GFLALFTHOSWQCRKISLETGAONIOMCTMLOSTFA-----EHLVQML-----S 288
DB 204 GLTYARTLRYLMRAVDPAAGSAGARRAKYTRMILIVAAFLCWMHMHALLICVMPGQ 263
QY 289 FPLAVGLFOLIDGLIYAAVGYTKR-----RLKNKKGKN-----S 324
DB 264 FPLTRATYAL---RILSHLVANSVCNPIYVALVSHHFKGFERTTCAGLGRAPGRAS 319
QY 325 GCTEVCHTRKSTSS-----RETNAFLEVNE-EGAITPGRPMDCHRALEP 369
DB 320 G--RVCAARGTSGSVLERESSDLHMSAAGALRPGRASQC--ILRP 366

RESULT 10

US-08-993-424B-7
; Sequence 7, Application US/08993424B

LENGTH: 835
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: CD97amino acid sequence encoded by full-length
US-09-284-819-6

Query Match 5.0%; Score 98; DB 4; Length 835;
Best Local Similarity 22.8%; Pred. No. 0.23;
Matches 74; Conservative 50; Mismatches 118; Indels 82; Gaps 19;

QY 67 GAVAGLCCFGIMPTAYLLAISFLKPYQ---AIAVLIMCCPGGITSNIETWVD-- 120
DB 554 GLALSLFLC--LLCLTLFL-----VRPIQSRTHHLHCLCLFVG--STIFLAGIENE 604
QY 121 -GDMDLISMTCTSVAAIGMPLCIYLYTWSW-SIQONLTPYONIGITVLCLTPVAF 178
DB 605 GGQVGL---RCRIYVA--GLLHYC-FLAALFCMSIE-----GLELYFLVAVRQ 646
QY 179 GYVAVRMPKSKIIKIGAVVGVLLVAVAVVLAAGVLAAGVLAAGVLAAGVLAAGVLAAGV 236
DB 647 GGLSTRW-----LCLIGY---GVPLLIVGSAIYSGYRPRYCWIDPEQFLMSFL 697
QY 237 GAVTGFEL---ALFTHQSWQRCRTISLETGAONIQMCTIMLQ---LSFTAEHLVOMLSF 289
DB 698 GVTFTIICNAVIFVTTWKLVOKPS-----EINPMKKLKKARALITTAQLPLGC 751
QY 290 PLAYGLFQIDGFLVAAVQT-----YKRLKNRHK-----KNSGCT 327
DB 752 TWVFGHFDRLSLVLTVFTVTLNCLQAFVLYLHCLNKKVREYRKVACLAVAGSKYS 811
QY 328 EYCHTRKSTSSRETNALFEVNEG 351
DB 812 EFTSTTSGTHNQTRA-LRASSG 834

RESULT 13

US-08-477-451-4
Sequence 4, Application US/08477451
Patent No. 592865
GENERAL INFORMATION:
APPLICANT: Covacci, Antonello
TITLE OF INVENTION: Helicobacter Pylori CagI Region
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,451
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McClung, Barbara G.
REGISTRATION NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 0335.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2708
TELEFAX: 510-655-3542
INFORMATION FOR SEQ. ID NO. 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 3177 amino acids
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-477-451-4

Query Match 4.9%; Score 96.5; DB 2; Length 3177;
Best Local Similarity 21.9%; Pred. No. 2.2;
Matches 56; Conservative 35; Mismatches 62; Indels 103; Gaps 12;

QY 106 CPGGISNIFFWDDGMDLSISMTCTSV-----AALGM-----MPLCIYLYT 149
DB 57 CLKAVLSLTFMWI---LISLNTVSVVKIRYSLGMPKLKLAITLGLPSCLRTF- 111
QY 150 WWSLQONLTPYONIGITVCL---TIPVAF---GVVAVRMPKSKIIKIGAVVGV 204
DB 112 ---LSSPLVWISNSFSVTLNLMWSERLPSPFLKKIFVGH---CSLIVSAIGAKRSVM 163
QY 205 LLVAVAGVLAAGVLAAGVLAAGVLAAGVLAAGVLAAGVLAAGVLAAGVLAAGVLAAGV 264
DB 164 L-----VASLTIAFLF-----LAVFS----- 179
QY 265 QNIQMCIT---MQLSFTAEHLVOMLSFPLAYGLFQIDGFLVAAVQYKRLKNKH 319
DB 180 ---NSLTATPFGSINTISRLHQLRYAHPLPLG-----YERKGNKR 219
QY 320 GKNSGCTEYCHTRKS 335
DB 220 AKHHYCLANLTHQROS 235

RESULT 14

US-08-956-322-4
Sequence 4, Application US/08956322
Patent No. 6277977
GENERAL INFORMATION:
APPLICANT: SATHE, GANESH
TITLE OF INVENTION: CDNA CLONE HAP0167 THAT ENCODES
TITLE OF INVENTION: A HUMAN 7-TRANSMEMBRANE RECEPTOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: RATNER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,322
FILING DATE: 23-OCT-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/049,329
FILING DATE: 11-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F.
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-70075
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
INFORMATION FOR SEQ. ID NO. 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 521 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-956-322-4

Query Match 4.9%; Score 96; DB 4; Length 521;
Best Local Similarity 19.3%; Pred. No. 0.19;
Matches 82; Conservative 52; Mismatches 107; Indels 184; Gaps 22;

4 NC---SSSSACPNSSSEELPVGLEVHGNLELFTVSTVMGLMFLSGCSVEIRKMS 60
203 NCSHLSFAVLMALTSQEDP-----VLTVITYV----- 221
61 HIRRPWGIAVGLCOGFLMPFTAYLLAIFSLKPVQAIIVLMGCCPGGTSNIFTFWD 120
232 ---GLSVSLC-----LLAALFTL-----CK-AIQNTST----- 258
121 GMDLISIMTCTVAALGMM-----PLC-----LYLTWSMSL----- 154
259 ---SLHQLSLCFLHMLFLVGLIDRTEPKVLSIIAGALHYLLAFLAFTMLEGVHLFL 315
155 -QONLT-IPYONIGITLVCLTIPVAGVYVNYRMPKOSKIIKIGAVGVLLVAVAG 212
316 TAANLTVVNVSSINRLMKIMFPVYG-----VPAVT 347
213 VVLAKGSM-----NSDITLLTI--SFIFLIGHVTGL--LALFTHOSW----- 252
348 VAISASWPHLYGTADRCWHLHDOGFMSFLGPVCAIFSANLVFLIVFILLRKLSLN 407
253 -----QRCRTISLETGAQ-----NIOWCITMQLSFTAEHLVOMLSFPLAYGLFOLID-- 300
408 SEVSTIQNRMFLAFKATAQLFILGCTWCLGLLQVPPAQ-----VMAY-LFTIINSI 458
301 -GFLIYAAVQTYRRLKKNHGK-----KNSGCFVCHTRKSTSSRETNALFVNEG 351
459 QGFIFLVYCLLSQVQVQKQKWFREIVKSKSESYTLSSKMGPDSPKS-----EG 510
QY 352 AIRPG 356
DB 511 DVPPG 515

RESULT 15
US-08-937-067-13
Sequence 13, Application US/08937067
Patent No. 6433155

GENERAL INFORMATION:
APPLICANT: Umanaky, Samuel
APPLICANT: Melkonyan, Hovsep
TITLE OF INVENTION: A FAMILY OF GENES ENCODING
TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
TITLE OF INVENTION: METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA

COUNTRY: USA
ZIP: 94304-1018

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Releasee #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,067.

FILING DATE:

CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:

NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943

REFERENCE/DOCKET NUMBER: 23647-20018.00

TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600

TELEFAX: (650) 494-0792

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:
LENGTH: 572 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-937-067-13

Query Match 4.9%; Score 96; DB 4; Length 572;
Best Local Similarity 21.9%; Pred. No. 0.22;
Matches 57; Conservative 40; Mismatches 79; Indels 84; Gaps 13;

40 VMGLMFLSGCSVEIRKMSHIRRPWGIAVGLCOGFLMPFTAYLLAIFSLKPVQ 96
337 LFMVLYFFFGMASSI---WVILSLTWFLAAGM--KMGHEALFANSQYFHLAAMAVPAVK 390
97 AIAVLIMGCCPGGTSNIFTFWDDMDLSIMTCTVAALG---MMPLCIYLYTWSMS 153
391 TITILAMG-----QVGDLSGVCYVGLSDVDAIRGFVLAFLFYLYF----- 432
154 LOONLTIPYONIGITLVCLTIPVAGV-----YVNYRMPKOSKIIKIGAVGVLLV 208
433 -----IGTSFLAGFVSLFRITIMHGDGTEKLEKLVRIQ--VFSVLYTVP 479
209 AVAGVLA-----KGSW-----NSDITLLTISIFPLI 236
480 AT--IVLACYFYEQAERHEMERTWLLQTCASYAVPCPRHFSPMSPDFVFMKYLMTMI 537
QY 237 -GHVTF-LLALFTHOSMOR 254
DB 538 VQITTFWIMSGKTLQSMR 557

Search completed: June 9, 2003, 07:10:42
Job time : 21 secs